

#5



PCT09

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/914,168

DATE: 03/13/2002
TIME: 13:41:30

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\03132002\1914168.raw

4 <110> APPLICANT: Ruelle, Jean-Louis
6 <120> TITLE OF INVENTION: IMMUNOGENIC COMPOUNDS
9 <130> FILE REFERENCE: BM45378
11 <140> CURRENT APPLICATION NUMBER: 09/914,168
C--> 12 <141> CURRENT FILING DATE: 2002-01-28
14 <150> PRIOR APPLICATION NUMBER: 9904559.3
15 <151> PRIOR FILING DATE: 1999-02-26
17 <150> PRIOR APPLICATION NUMBER: PCT/EP00/01468
18 <151> PRIOR FILING DATE: 2000-02-23
20 <160> NUMBER OF SEQ ID NOS: 6
22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2760
26 <212> TYPE: DNA
27 <213> ORGANISM: Moraxella catarrhalis
29 <400> SEQUENCE: 1
30 atgtcaaaggc cggtttgtt tgcaaatcgcc agttttatgc ctgtcgccatt ggcggcatt 60
31 ttgccttgc tgacatcgca agcattggca caacaaaata accctgcaaa catcatcaat 120
32 catgtaccccg ctcatgacac cgccatcaat caagcaaagg caggcaatcc gcctgtttg 180
33 ctaacacctg agcagataca agcacgcctt aatgctgtg gactgaatgc taagcccaa 240
34 tcacaagctt tggatgttgtt caatttgtat gatcaatcgcc cgatatctcg tatcggtgag 300
35 caatcaccctt ctttgggtt ggatatgtcg gtcatcgaaag aaaccacacc gctaagctt 360
36 gaggaattat ttgctcaaga atctactgag atggaaatca atccaaatgaa ttatattcca 420
37 gaatatcaag gcgagcaacc taatagttagt gttgggtgtac caccgacatt agaacctgaa 480
38 aaaccagggtt tgatcaagcg tcctttagcgc cgcctattta atgatgggtt caataaggtg 540
39 cctaggctta aggcaaaattt ttatcaatca tcgcaatcag gcggaaaccagg tgcgattggg 600
40 tcatcgcatc aaaaaacaga gccttatgca aatatacgaa cagcacttgc agacatcacc 660
41 caagagtcaag cgatggattt gaatggctt atccccacgc taaggcaaaatc tgctttggg 720
42 gcagcgcgtt ctgtcggtt ttatgatattt gatttatcaa tcataagaaa tagcatcgga 780
43 gaggtggatg tcatcatcctt tgatttagt gaacctgtttt atattgatta tcgagcgtt 840
44 gaggtacgag gtgaagggtgc tgatgataaa gcattttacta ccgtggcgga tgaggtgcca 900
45 ttgctgtatcg gcgatgtctt tcatacatggc aagtacgaaa caaaaaaaaa tctcatcgaa 960
46 aatgccatgt ctgaacatgg atatggat gggcgttgc tggatcggtt agttgtatgt 1020
47 attttgcacatgttataatccgc tgatgtcagg ttaattttatg atacaggtac gcagtatcg 1080
48 tttgtatggg tggtatgtt taccattgtat cctaaaaacca atcaatttgc aaccgatcca 1140
49 gataagctgc cagttaaacg agaattactt gagcagttac tcaccgttacatggggagag 1200
50 gcttacaattt tacaggcggtt gctgtcactt tcaaatgatt tgattggccac acggttttt 1260
51 aatatggtga ataccgagat tgccttcca gagcgtgaac agatccaaaaa cgaccaagtgc 1320
52 agcttgcgttgc agtcttcaag tagccgtactt gaaccacac aagttgtatgc aagcacactt 1380
53 gaacctgtca ttgaaaccgt tgagctaaacg gatggggatataatggat ttcgcccattc 1440
54 gaatttagtgc catctaatctt gattcaagac aagctaaattt tggtggctgc caaggctgc 1500
55 catttatatg acatgcctgttgatgggtt cttgcccattca atcatgtatgc tggcgtaaat 1560
56 cgctctatgtt tggcagaat cagcgatgccc gatctgtccq ttgcacgtgc tattttacct 1620

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108	195	200	205
109	Tyr Ala Asn Ile Lys Ala Ala	Leu Glu Asp Ile	Thr Gln Glu Ser Ala
110	210	215	220
111	Met Asp Leu Asn Gly Ser	Ile Pro Arg Leu Arg	Gln Thr Ala Leu Val
112	225	230	235
113	Ala Ala Arg Ala Val Gly	Tyr Tyr Asp Ile Asp	Leu Ser Ile Ile Arg
114	245	250	255
115	Asn Ser Ile Gly Glu Val Asp	Val Ile Ile His Asp	Leu Gly Glu Pro
116	260	265	270
117	Val Tyr Ile Asp Tyr Arg Ala	Val Glu Val Arg Gly	Glu Gly Ala Asp
118	275	280	285
119	Asp Lys Ala Phe Thr Thr Val	Ala Asp Glu Val	Pro Leu Leu Ile Gly
120	290	295	300
121	Asp Val Phe His His Gly	Lys Tyr Glu Thr Lys	Lys Asn Leu Ile Glu
122	305	310	315
123	Asn Ala Ser Ala Glu His	Gly Tyr Phe Asp	Gly Arg Trp Leu Asp Arg
124	325	330	335
125	Ser Val Asp Val Ile Leu Pro Asp	Asn Thr Ala Asp Val	Ser Leu Ile
126	340	345	350
127	Tyr Asp Thr Gly Thr Gln Tyr Arg	Phe Asp Glu Val Val	Phe Phe Thr
128	355	360	365
129	Ile Asp Pro Lys Thr Asn Gln	Leu Thr Thr Asp	Pro Asp Lys Leu Pro
130	370	375	380
131	Val Lys Arg Glu Leu Leu Glu Gln	Leu Leu Thr Val Asn	Met Gly Glu
132	385	390	395
133	Ala Tyr Asn Leu Gln Ala Val Arg	Ala Leu Ser Asn	Asp Leu Ile Ala
134	405	410	415
135	Thr Arg Tyr Phe Asn Met Val Asn	Thr Glu Ile Val Phe	Pro Glu Arg
136	420	425	430
137	Glu Gln Ile Gln Asn Asp Gln Val	Ser Phe Glu Gln	Ser Ser Ser
138	435	440	445
139	Arg Thr Glu Pro Ala Gln Val Asp	Glu Ser Thr Leu	Glu Pro Val Ile
140	450	455	460
141	Glu Thr Val Glu Leu Thr Asp Gly	Ile Leu Met Asp Ile	Ser Pro Ile
142	465	470	475
143	Glu Phe Ser Ala Ser Asn Leu	Ile Gln Asp Lys	Leu Asn Leu Val Ala
144	485	490	495
145	Ala Lys Ala Arg His Leu Tyr Asp	Met Pro Asp Asp Arg	Val Leu Ala
146	500	505	510
147	Ile Asn His Asp Asp Gly Val Asn	Arg Ser Ile Leu	Gly Arg Ile Ser
148	515	520	525
149	Asp Ala Val Ser Ala Val Ala	Arg Ala Ile Leu	Pro Asp Glu Ser Glu
150	530	535	540
151	Asn Glu Val Ile Asp Leu Pro	Glu Arg Thr Ala	Leu Ala Asn Arg Lys
152	545	550	555
153	Thr Pro Ala Asp Val Tyr Gln	Ser Lys Lys Val	Pro Leu Tyr Val Phe
154	565	570	575
155	Val Ala Ser Asp Lys Pro Arg Asp	Gly Gln Ile	Gly Leu Gly Trp Gly
156	580	585	590

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157 Ser Asp Thr Gly Thr Arg Leu Val Thr Lys Phe Glu His Asn Leu Ile
158 595 600 605
159 Asn Arg Asp Gly Tyr Gln Ala Gly Ala Glu Leu Arg Leu Ser Glu Asp
160 610 615 620
161 Lys Lys Gly Val Lys Leu Tyr Ala Thr Lys Pro Leu Ser His Pro Leu
162 625 630 635 640
163 Asn Asp Gln Leu Arg Ala Thr Leu Gly Tyr Gln Gln Glu Val Phe Gly
164 645 650 655
165 His Ser Thr Asn Gly Phe Asp Leu Ser Thr Arg Thr Leu Glu His Glu
166 660 665 670
167 Ile Ser Arg Ser Ile Ile Gln Asn Gly Gly Trp Asn Arg Thr Tyr Ser
168 675 680 685
169 Leu Arg Tyr Arg Leu Asp Lys Leu Lys Thr Gln Ala Pro Pro Glu Thr
170 690 695 700
171 Trp Gln Asp Leu Pro Val Asp Phe Val Asn Gly Lys Pro Ser Gln Glu
172 705 710 715 720
173 Ala Leu Leu Ala Gly Val Ala Val His Lys Thr Val Ala Asp Asn Leu
174 725 730 735
175 Val Asn Pro Met Arg Gly Tyr Arg Gln Arg Tyr Ser Leu Glu Val Gly
176 740 745 750
177 Ser Ser Gly Leu Val Ser Asp Ala Asn Met Ala Ile Ala Arg Ala Gly
178 755 760 765
179 Ile Ser Gly Val Tyr Ser Phe Gly Asp Asn Ala Tyr Gly Ser Asn Arg
180 770 775 780
181 Ala His Gln Met Thr Gly Gly Ile Gln Ala Gly Tyr Ile Trp Ser Asp
182 785 790 795 800
183 Asn Phe Asn His Val Pro Tyr Arg Leu Arg Phe Phe Ala Gly Gly Asp
184 805 810 815
185 Gln Ser Ile Arg Gly Tyr Ala His Asp Ser Leu Ser Pro Ile Ser Asp
186 820 825 830
187 Lys Gly Tyr Leu Thr Gly Gly Gln Val Leu Ala Val Gly Thr Ala Glu
188 835 840 845
189 Tyr Asn Tyr Glu Phe Met Lys Asp Leu Arg Leu Ala Val Phe Gly Asp
190 850 855 860
191 Ile Gly Asn Ala Tyr Asp Lys Gly Phe Thr Asn Asp Thr Lys Ile Gly
192 865 870 875 880
193 Ala Gly Val Gly Val Arg Trp Ala Ser Pro Val Gly Gln Val Arg Val
194 885 890 895
195 Asp Val Ala Thr Gly Val Lys Glu Glu Gly Asn Pro Ile Lys Leu His
196 900 905 910
197 Phe Phe Ile Gly Thr Pro Phe
198 915
200 <210> SEQ ID NO: 3
201 <211> LENGTH: 2670
202 <212> TYPE: DNA
203 <213> ORGANISM: Moraxella catarrhalis
205 <400> SEQUENCE: 3
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207 caagcaaagg caggcaatcc gcctgttttg ctaacacctg agcagataca agcacgcctt 120

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208	aatgctgctg	gactgaatgc	taagcccaa	tcacaagctt	tggatgtgt	caatttgat	180								
209	gatcaatcg	cgatatctcg	tatcggtgag	caatcaccc	cttggg	tttggatgtcg	240								
210	gtcatcgaa	aaaccacacc	gctaagctt	gaggaattat	ttgctcaaga	atctactgag	300								
211	atggaaatca	atccaaatga	ttatattcca	gaatatcaag	gcgagcaacc	taatagttag	360								
212	gtggttgtac	caccgacatt	agaacctgaa	aaaccagg	ttgatcaagcg	tctttatgca	420								
213	cgcctattt	atgatgggt	caataagg	cctaggctt	aggcaaattt	ttatcaatca	480								
214	tcgcaatcag	gcgaaaccag	tgcgattggg	tcatcgatc	aaaaa	acaga	540								
215	aatatcaa	agcacttga	agacatcacc	caagagt	cgatggattt	gaatggctct	600								
216	atcccacg	cc	taaggcaa	ac	tgcttgg	gcagcgcgt	660								
217	gatttatcaa	tcataagaaa	tagcatcg	gagg	tttgc	tgat	720								
218	gaacctgtt	atattgatta	tcgagcggt	gagg	tacg	gtgatgataaa	780								
219	gcatttacta	ccgtggc	g	tgagg	tgatgt	gcgatgtctt	840								
220	aagtacgaa	ccaaaaaaa	tctcatcgaa	aatg	ccag	tgatgt	900								
221	gggcgttggc	tggatcg	tttgc	at	tttgc	at	960								
222	ttaatttat	atacagg	tac	gcagtatcg	tttgc	tgatatttt	1020								
223	cctaaaacca	atcaattgac	aaccgatc	gataa	gctgc	cagttaaac	1080								
224	gagcagttac	tcaccgtt	aa	catgggag	gctt	acaatt	1140								
225	tcaa	atgttgc	ac	cggtat	ttt	aatatgg	1200								
226	gagcgtgaa	ac	agatccaaa	cgacca	agg	tgcttgc	1260								
227	gaaccagc	ac	aagt	tgat	ga	agcactt	1320								
228	gatggat	at	at	ttc	ccc	catcg	1380								
229	aagctaa	att	ttgtgg	ctgc	caagg	ctgc	1440								
230	cttgc	at	cat	gat	gta	tttgc	1500								
231	gtatctg	cc	ttgc	acgt	tttgc	at	1560								
232	cccgagc	gt	ccg	catt	ggc	at	1620								
233	gttgc	ctat	at	gttgc	tttgc	at	1680								
234	tgggatc	gg	acacagg	gt	tttgc	at	1740								
235	gatgg	ctatc	aagcagg	gc	tttgc	at	1800								
236	tatgc	ccacca	aaccg	cttgc	tttgc	at	1860								
237	caaca	agaag	ttttgg	tca	tttgc	at	1920								
238	catgagat	tttgc	tttgc	tttgc	tttgc	at	1980								
239	tatcg	tcttgc	ata	gctt	tttgc	at	2040								
240	gat	tttgc	tca	atggta	tttgc	tttgc	2100								
241	acgg	tttgc	ca	gat	tttgc	at	2160								
242	gttgg	ctcaa	gcgg	tttgc	tttgc	at	2220								
243	ggcgtgt	tata	ttttgg	tttgc	tttgc	at	2280								
244	ggcata	caag	cagg	at	tttgc	at	2340								
245	tttttgc	gtgg	cgacca	aagt	tttgc	at	2400								
246	tca	gataagg	gtt	atcg	tttgc	at	2460								
247	tatgaa	tttgc	tttgc	tttgc	tttgc	at	2520								
248	aaagg	cttgc	tttgc	tttgc	tttgc	at	2580								
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253	<211>	LENGTH:	889												
254	<212>	TYPE:	PRT												
255	<213>	ORGANISM:	Moraxella catarrhalis												
257	<400>	SEQUENCE:	4												
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/914,168

DATE: 03/13/2002

TIME: 13:41:31

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03132002\I914168.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date